



results of BLAST

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1089315578-5719-187285618589.BLASTQ4

Query=

(49 letters)

Database: All non-redundant GenBank CDS

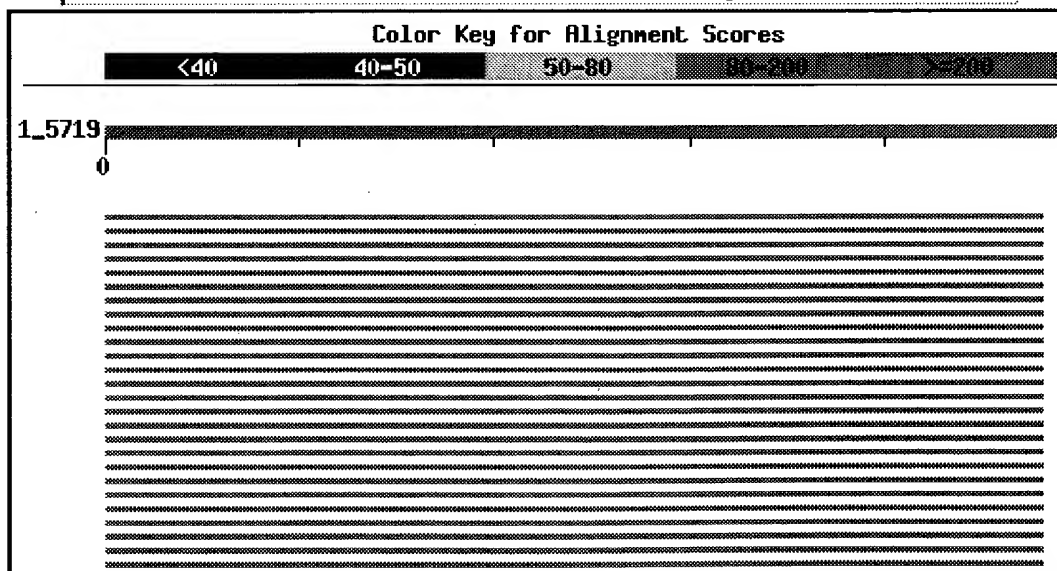
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
1,921,076 sequences; 640,719,545 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 172 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

[gi|1370092|emb|CAA65449.1|](#) kinase [Gallus gallus]

Score E
(bits) Value

95 2e-19

gi 7512236 pir T28145 RING3 kinase - chicken > gi 3129967 e...	<u>95</u>	3e-19	
gi 2995270 emb CAA15819.1 MMRING3.1.2 [Mus musculus] > gi 3...	<u>95</u>	3e-19	L
gi 47059183 ref NP_997660.1 bromodomain-containing 2 [Ratt...	<u>95</u>	3e-19	L
gi 34392374 dbj BAC82511.1 Serine threonine Kinase [Coturn...	<u>95</u>	3e-19	
gi 6753910 ref NP_034368.1 bromodomain containing 2; femal...	<u>95</u>	3e-19	L
gi 2995269 emb CAA15818.1 MMRING3.1.1 [Mus musculus]	<u>94</u>	4e-19	L
gi 1588281 prf 2208296A RING3 protein	<u>94</u>	5e-19	
gi 39645317 gb AAH63840.1 BRD2 protein [Homo sapiens]	<u>94</u>	5e-19	L
gi 15706262 emb CAC69991.1 O14.1.1 (bromodomain-containing...	<u>94</u>	5e-19	L
gi 4826806 ref NP_005095.1 bromodomain containing protein ...	<u>94</u>	5e-19	L
gi 12802525 gb AAK07919.1 ring 3 [Mus musculus]	<u>94</u>	7e-19	L
gi 2780775 dbj BAA24377.1 Ring3 [Mus musculus]	<u>93</u>	8e-19	L
gi 1082363 pir A56619 female sterile homeotic (fsh) homolo...	<u>93</u>	8e-19	L
gi 1370115 emb CAA65450.1 kinase [Homo sapiens]	<u>93</u>	8e-19	L
gi 2780777 dbj BAA24378.1 Ring3 [Mus musculus] > gi 2780779...	<u>93</u>	1e-18	L
gi 27696271 gb AAH43784.1 Brd2-A-prov protein [Xenopus lae...	<u>90</u>	1e-17	L
gi 120558 sp P13709 FSH_DROME FEMALE STERILE HOMEOTIC PROTE...	<u>89</u>	2e-17	L
gi 24640482 ref NP_511078.2 CG2252-PB [Drosophila melanoga...	<u>89</u>	2e-17	L
gi 33416865 gb AAH55543.1 Unknown (protein for IMAGE:59138...	<u>87</u>	6e-17	
gi 27804346 gb AAO22237.1 BRD4-NUT fusion oncoprotein [Hom...	<u>87</u>	9e-17	
gi 24640484 ref NP_727228.1 CG2252-PA [Drosophila melanoga...	<u>87</u>	9e-17	L
gi 31206311 ref XP_312107.1 ENSANGP00000016848 [Anopheles ...	<u>87</u>	1e-16	
gi 34853148 ref XP_342397.1 similar to Brd3 protein [Rattu...	<u>86</u>	2e-16	L
gi 48134425 ref XP_393347.1 similar to ENSANGP00000016848 ...	<u>86</u>	2e-16	L
gi 26332152 dbj BAC29806.1 unnamed protein product [Mus mu...	<u>85</u>	3e-16	L
gi 47115837 sp Q8K2F0 BRD3_MOUSE Bromodomain-containing pro...	<u>85</u>	3e-16	L
gi 31981064 ref NP_075825.2 bromodomain containing 3; brom...	<u>85</u>	3e-16	L
gi 8575733 gb AAF78072.1 bromodomain-containing FSH-like p...	<u>85</u>	3e-16	L
gi 40788944 dbj BAA05393.2 KIAA0043 [Homo sapiens]	<u>85</u>	4e-16	L
gi 21594670 gb AAH32124.1 BRD3 protein [Homo sapiens]	<u>85</u>	4e-16	L
gi 26345416 dbj BAC36359.1 unnamed protein product [Mus mu...	<u>85</u>	4e-16	L
gi 11067749 ref NP_031397.1 bromodomain containing protein...	<u>85</u>	4e-16	L
gi 3184498 gb AAC27978.1 R31546_1 [Homo sapiens]	<u>83</u>	1e-15	L
gi 37674287 ref NP_932762.1 bromodomain containing 4 isofo...	<u>83</u>	1e-15	L
gi 7657218 ref NP_055114.1 bromodomain-containing protein ...	<u>83</u>	1e-15	L
gi 45501005 gb AAH67129.1 Unknown (protein for IMAGE:61387...	<u>82</u>	2e-15	
gi 33879612 gb AAH30158.1 BRD4 protein [Homo sapiens]	<u>82</u>	2e-15	L
gi 33416361 gb AAH55533.1 Zgc:77289 protein [Danio rerio]	<u>82</u>	2e-15	L
gi 47086635 ref NP_997867.1 Unknown (protein for MGC:77289...	<u>82</u>	3e-15	L
gi 33417197 gb AAH55508.1 Unknown (protein for IMAGE:38191...	<u>82</u>	3e-15	
gi 47216871 emb CAG11678.1 unnamed protein product [Tetrao...	<u>82</u>	3e-15	
gi 19171509 emb CAC84085.1 hypothetical protein [Takifugu ...	<u>81</u>	6e-15	
gi 34862361 ref XP_343176.1 similar to bromodomain-contain...	<u>80</u>	7e-15	L
gi 19718731 ref NP_490597.1 bromodomain-containing protein...	<u>80</u>	8e-15	L
gi 9931486 gb AAG02191.1 cell proliferation related protei...	<u>80</u>	9e-15	L
gi 31560788 ref NP_065254.2 bromodomain containing 4 isofo...	<u>80</u>	9e-15	L
gi 47210026 emb CAF90901.1 unnamed protein product [Tetrao...	<u>80</u>	1e-14	
gi 18157527 dbj BAB83842.1 BRD2~partially supported by GEN...	<u>79</u>	2e-14	

gi 47212213 emb CAF94980.1 	unnamed protein product [Tetrao...	78	3e-14	
gi 49118460 gb AAH73443.1 	Unknown (protein for IMAGE:55162...	78	3e-14	
gi 38014413 gb AAH60452.1 	LOC398944 protein [Xenopus laevis]	78	4e-14	L
gi 24210305 emb CAD54663.1 	SI:dZ12F11.5 (bromodomain-conta...	77	8e-14	L
gi 16905089 ref NP_473395.1 	bromodomain, testis-specific; ...	76	2e-13	L
gi 10441758 gb AAG17179.1 	RING3 [Myxine glutinosa]	76	2e-13	
gi 47209011 emb CAF91369.1 	unnamed protein product [Tetrao...	76	2e-13	
gi 49899749 gb AAH76786.1 	Unknown (protein for MGC:83700) ...	75	3e-13	
gi 28278510 gb AAH45866.1 	Similar to bromodomain containin...	75	3e-13	
gi 33355659 gb AAQ16198.1 	testis-specific BRDT protein [Ho...	75	4e-13	L
gi 46399198 ref NP_001717.2 	testis-specific bromodomain pr...	75	5e-13	L
gi 28839607 gb AAH47900.1 	BRDT protein [Homo sapiens]	74	5e-13	L
gi 2554915 gb AAB87862.1 	BRDT [Homo sapiens]	74	5e-13	L
gi 34875962 ref XP_223146.2 	similar to bromodomain-contain...	74	7e-13	L
gi 20302741 gb AAM18869.1 	unknown [Branchiostoma floridae]	73	1e-12	
gi 38541875 gb AAH62700.1 	BRDT protein [Homo sapiens]	72	3e-12	L
gi 47210344 emb CAF96012.1 	unnamed protein product [Tetrao...	67	1e-10	
gi 15242727 ref NP_201138.1 	DNA-binding bromodomain-contai...	65	2e-10	
gi 19528091 gb AAL90160.1 	AT24535p [Drosophila melanogaster]	64	7e-10	L
gi 7485801 pir T00472	probable RING3 protein [imported] - ...	63	2e-09	
gi 30686240 ref NP_181036.2 	DNA-binding bromodomain-contai...	62	2e-09	
gi 17551634 ref NP_508124.1 	kinase (40.9 kD) (XB213) [Caen...	62	4e-09	L
gi 15219397 ref NP_177458.1 	DNA-binding bromodomain-contai...	61	6e-09	
gi 47208417 emb CAF92198.1 	unnamed protein product [Tetrao...	61	6e-09	
gi 42407711 dbj BAD08859.1 	putative bromodomain-containing...	61	7e-09	
gi 24649433 ref NP_651190.1 	CG13597-PA [Drosophila melanog...	60	7e-09	L
gi 39592569 emb CAE63646.1 	Hypothetical protein CBG08144 [...	60	9e-09	
gi 42571057 ref NP_973602.1 	DNA-binding bromodomain-contai...	60	1e-08	
gi 17064912 gb AAL32610.1 	Unknown protein [Arabidopsis tha...	60	1e-08	
gi 9294219 dbj BAB02121.1 	unnamed protein product [Arabido...	59	2e-08	
gi 15232127 ref NP_189362.1 	DNA-binding bromodomain-contai...	59	2e-08	
gi 17510957 ref NP_491384.1 	bromodomain containing protein...	59	2e-08	L
gi 32564850 ref NP_871879.1 	bromodomain containing protein...	59	3e-08	L
gi 18394534 ref NP_564037.1 	DNA-binding bromodomain-contai...	58	3e-08	
gi 39582126 emb CAE60803.1 	Hypothetical protein CBG04495 [...	58	4e-08	
gi 47201045 emb CAF89147.1 	unnamed protein product [Tetrao...	58	4e-08	
gi 17568247 ref NP_509771.1 	bromodomain protein (XL193) [C...	58	4e-08	L
gi 11358472 pir T48600	kinase-like protein - Arabidopsis t...	58	4e-08	
gi 8885596 dbj BAA97526.1 	unnamed protein product [Arabido...	58	5e-08	
gi 30694987 ref NP_199467.2 	DNA-binding bromodomain-contai...	58	5e-08	
gi 34852199 ref XP_238186.2 	similar to MMRING3.1.1 [Rattus...	58	5e-08	L
gi 25511645 pir H86312	F2H15.2 protein - Arabidopsis thali...	58	5e-08	
gi 42568797 ref NP_201366.3 	DNA-binding bromodomain-contai...	58	5e-08	
gi 18417335 ref NP_568297.1 	DNA-binding bromodomain-contai...	58	5e-08	
gi 8978291 dbj BAA98182.1 	unnamed protein product [Arabido...	58	5e-08	
gi 7504519 pir T22845	hypothetical protein F57C7.1a - Caen...	57	6e-08	
gi 15810439 gb AAL07107.1 	unknown protein [Arabidopsis tha...	57	6e-08	
gi 25152243 ref NP_509770.2 	bromodomain containing (XL193)...	57	6e-08	L
gi 18395937 ref NP_566151.1 	DNA-binding bromodomain-contai...	57	7e-08	
gi 6016737 gb AAF01563.1 	hypothetical protein [Arabidopsis...	57	1e-07	
gi 34903950 ref NP_913322.1 	putative PSTVd RNA-biding prot...	56	1e-07	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|1370092|emb|CAA65449.1| kinase [Gallus gallus]
Length = 729

Score = 95.9 bits (237), Expect = 2e-19
Identities = 46/49 (93%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRR LE++Y
Sbjct: 40 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRR-LENNY 87

Score = 59.3 bits (142), Expect = 2e-08
Identities = 26/41 (63%), Positives = 32/41 (78%)

Query: 9 FAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
+AWPF +PVDA LGL DYH+IIK PMD+ TIKR++ DY
Sbjct: 315 YAWPFYKPVDAALGLHDYHEIIKHPMDLSTIKRKMEENRDY 355

☐ >gi|7512236|pir||T28145 RING3 kinase - chicken
gi|3129967|emb|CAA18965.1| RING3 kinase [synthetic construct]
Length = 733

Score = 95.5 bits (236), Expect = 3e-19
Identities = 46/49 (93%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRR LE++Y
Sbjct: 40 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRR-LENNY 87

Score = 58.9 bits (141), Expect = 3e-08
Identities = 26/41 (63%), Positives = 32/41 (78%)

Query: 9 FAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
+AWPF +PVDA LGL DYH+IIK PMD+ TIKR++ DY
Sbjct: 319 YAWPFYKPVDAALGLHDYHEIIKHPMDLSTIKRKMEENRDY 359

☐ >gi|2995270|emb|CAA15819.1| ☒ MMRING3.1.2 [Mus musculus]
gi|3041763|dbj|BAA25416.1| ☒ Ring3 [Mus musculus]
gi|3811391|gb|AAC69907.1| ☒ RING3 [Mus musculus]
Length = 798

Score = 95.5 bits (236), Expect = 3e-19
Identities = 46/49 (93%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRR LE++Y
Sbjct: 86 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRR-LENNY 133

Score = 57.8 bits (138), Expect = 7e-08
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 367 YAWPFYKPVDASALGLHDYHDIKHPMDLSTVKRKMENRDY 407

☐ >gi|47059183|ref|NP_997660.1| ☒ bromodomain-containing 2 [Rattus norvegicus]
gi|46237556|emb|CAE83937.1| ☒ bromodomain-containing 2 [Rattus norvegicus]
Length = 798

Score = 95.5 bits (236), Expect = 3e-19
Identities = 46/49 (93%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRR LE++Y
Sbjct: 86 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRR-LENNY 133

Score = 57.8 bits (138), Expect = 7e-08
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 367 YAWPFYKPVDASALGLHDYHDIKHPMDLSTVKRKMENRDY 407

☐ >gi|34392374|dbj|BAC82511.1| Serine threonine Kinase [Coturnix japonica]
Length = 735

Score = 95.5 bits (236), Expect = 3e-19
Identities = 46/49 (93%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRR LE++Y
Sbjct: 40 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRR-LENNY 87

Score = 58.9 bits (141), Expect = 3e-08
Identities = 26/41 (63%), Positives = 32/41 (78%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVDA LGL DYH+IIK PMD+ TIKR++ DY
Sbjct: 319 YAWPFYKPVDASALGLHDYHEIIKHPMDLSTIKRKMENRDY 359

☐ >gi|6753910|ref|NP_034368.1| ☒ bromodomain containing 2; female sterile homeotic
bromodomain-containing 2 [Mus musculus]
gi|3273701|gb|AAC24810.1| ☒ female sterile homeotic-related protein Frg-1 [Mus mu

Length = 798

Score = 95.5 bits (236), Expect = 3e-19

Identities = 46/49 (93%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRRLLLEDDY 49
MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRR LE++Y
Sbjct: 86 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRR-LENNY 133

Score = 57.8 bits (138), Expect = 7e-08

Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRRLLLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 367 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 407

☐ >[gi|2995269|emb|CAA15818.1|](#) ☒ MMRING3.1.1 [Mus musculus]
Length = 752

Score = 94.7 bits (234), Expect = 4e-19

Identities = 46/49 (93%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRRLLLEDDY 49
MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRR LE++Y
Sbjct: 40 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRR-LENNY 87

Score = 57.4 bits (137), Expect = 8e-08

Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRRLLLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 361

☐ >[gi|1588281|prf||2208296A](#) RING3 protein
Length = 509

Score = 94.7 bits (234), Expect = 5e-19

Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRRLLLEDDY 49
MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRR + Y
Sbjct: 40 MKALWKHQFAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRRLENNYY 88

Score = 57.4 bits (137), Expect = 9e-08

Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFRRQPVDAVKLGGLPDYHKIIKQPMMDGTIKRRLLLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 203 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 243

☐ >gi|39645317|gb|AAH63840.1| ☒ BRD2 protein [Homo sapiens]
Length = 836

Score = 94.7 bits (234), Expect = 5e-19
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
MKALWKHQFAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRRL + Y
Sbjct: 87 MKALWKHQFAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLENNYY 135

Score = 57.4 bits (137), Expect = 9e-08
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 368 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 408

☐ >gi|15706262|emb|CAC69991.1| ☒ O14.1.1 (bromodomain-containing protein 2 (RING3,
isoform 1) [Homo sapiens]
gi|15706263|emb|CAC69989.1| ☒ O27.1.1 (bromodomain-containing protein 2 (RING3, KIA
isoform 1) [Homo sapiens]
Length = 801

Score = 94.7 bits (234), Expect = 5e-19
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
MKALWKHQFAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRRL + Y
Sbjct: 87 MKALWKHQFAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLENNYY 135

Score = 57.4 bits (137), Expect = 9e-08
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFRQPVDAVKLGGLPDYHKIIKQPMDMGTIKRRLLLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 368 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 408


☐ >gi|4826806|ref|NP_005095.1| ☒ bromodomain containing protein 2; female sterile
gene 1; bromodomain-containing 2 [Homo sapiens]
gi|12230989|sp|P25440|BRD2 HUMAN ☒ Bromodomain-containing protein 2 (RING3 protei
gi|577293|dbj|BAA07641.1| ☒ KIAA9001 [Homo sapiens]
gi|2980663|emb|CAA43996.1| ☒ FSH [Homo sapiens]
Length = 801

Score = 94.7 bits (234), Expect = 5e-19
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRL + Y
Sbjct: 87 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYY 135

Score = 57.4 bits (137), Expect = 9e-08
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 368 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 408


☐ >gi|12802525|gb|AAK07919.1|  ring 3 [Mus musculus]
Length = 503

Score = 94.4 bits (233), Expect = 7e-19
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRL + Y
Sbjct: 86 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYY 134

Score = 57.0 bits (136), Expect = 1e-07
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 367 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 407


☐ >gi|2780775|dbj|BAA24377.1|  Ring3 [Mus musculus]
Length = 549

Score = 94.0 bits (232), Expect = 8e-19
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRL + Y
Sbjct: 86 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYY 134

Score = 57.0 bits (136), Expect = 1e-07
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 367 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDY 407

☐ >gi|1082363|pir||A56619 female sterile homeotic (fsh) homolog RING3 - human
gi|182769|gb|AAA68890.1|  putative

Length = 754

Score = 94.0 bits (232), Expect = 8e-19
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLEDDY 49
MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRL + Y
Sbjct: 40 MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLENNYY 88

Score = 57.0 bits (136), Expect = 1e-07
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPPMDLSTVKKRMENRDY 361

☐ >gi|1370115|emb|CAA65450.1| ☒ kinase [Homo sapiens]
Length = 754

Score = 94.0 bits (232), Expect = 8e-19
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLEDDY 49
MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRL + Y
Sbjct: 40 MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLENNYY 88

Score = 57.0 bits (136), Expect = 1e-07
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPPMDLSTVKKRMENRDY 361

☐ >gi|2780777|dbj|BAA24378.1| ☒ Ring3 [Mus musculus]
gi|2780779|dbj|BAA24379.1| ☒ Ring3 [Mus musculus]
Length = 503

Score = 93.2 bits (230), Expect = 1e-18
Identities = 45/49 (91%), Positives = 46/49 (93%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLEDDY 49
MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRL + Y
Sbjct: 40 MKALWKHQFAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLENNYY 88

Score = 56.6 bits (135), Expect = 1e-07
Identities = 25/41 (60%), Positives = 31/41 (75%)

Query: 9 FAWPFQPVDAVKLGDPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++ DY

Sbjct: 321 YAWPFYKPVVDASALGLHDYHDIKHPMDLSTVKKRMENRDY 361

☐ >gi|27696271|gb|AAH43784.1| ☒ Brd2-A-prov protein [Xenopus laevis]
Length = 539

Score = 90.5 bits (223), Expect = 1e-17
Identities = 41/49 (83%), Positives = 48/49 (97%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K+LWKHQF+WPFQPVDAVKLGLPDYHKIIKQPMDMGT+K+R LE++Y
Sbjct: 87 VKSLWKHQFSWPFQPVDAVKLGLPDYHKIIKQPMDMGTVKKR-LENNY 134

Score = 52.0 bits (123), Expect = 4e-06
Identities = 22/36 (61%), Positives = 28/36 (77%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRL 44
+AWPF +PVD LGL DY+ IIK PMDM TIK+++
Sbjct: 362 YAWPFYKPVDSALGLHDYDIKHPMDMSTIKKKM 397

☐ >gi|120558|sp|P13709|FSH_DROME FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION
PROTEIN)
gi|280611|pir||A43742 female sterile homeotic protein, 205K - fruit fly (Drosoph
melanogaster)
gi|157453|gb|AAA28540.1| ☒ 7.6 kb fsh membrane protein
Length = 2038

Score = 89.7 bits (221), Expect = 2e-17
Identities = 38/49 (77%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
MK +WKH F+WPF+QPVDA KL LPDYHKIIKQPMDMGTIK+R LE++Y
Sbjct: 47 MKVIWKHHFSWPFQPVDAKKLNLDPYHKIIKQPMDMGTIKKR-LENNY 94

Score = 62.8 bits (151), Expect = 2e-09
Identities = 27/45 (60%), Positives = 35/45 (77%), Gaps = 1/45 (2%)

Query: 6 KHQ-FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
KH +AWPF +PVDA LGL DYH IIK+PMD+GT+KR++ +Y
Sbjct: 495 KHSGYAWPFYKPVDAEMLGLHDYHDIKKPMDLGTVKKRMNDREY 539

☐ >gi|24640482|ref|NP_511078.2| ☒ CG2252-PB [Drosophila melanogaster]
gi|22831925|gb|AAF46312.3| ☒ CG2252-PB [Drosophila melanogaster]
Length = 2038

Score = 89.7 bits (221), Expect = 2e-17
Identities = 38/49 (77%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49

MK +WKH F+WPF+QPVDA KL LPDYHKIIKQPMDMGTIK+R LE++Y
Sbjct: 47 MKVIWKHHFWSWPFQQPVDAKLNLPDYHKIIKQPMDMGTIKKR-LENNY 94

Score = 62.8 bits (151), Expect = 2e-09
Identities = 27/45 (60%), Positives = 35/45 (77%), Gaps = 1/45 (2%)

Query: 6 KHQ-FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
KH +AWPF +PVDA LGL DYH IIK+PMD+GT+KR++ +Y
Sbjct: 495 KHSGYAWPFYKPVDAEMLGLHDYHDIKKPMDLGTVKKMDNREY 539

☐ >gi|33416865|gb|AAH55543.1| Unknown (protein for IMAGE:5913826) [Danio rerio]
Length = 515

Score = 87.8 bits (216), Expect = 6e-17
Identities = 39/44 (88%), Positives = 41/44 (93%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRL 44
+K LWKHQFAWPF QPVDAVKLGLPDYHKIIK PMDMGTIK+RL
Sbjct: 43 VKTLWKHQFAWPFYQPVDAVKLGLPDYHKIIKNPMDMGTIKKRL 86

Score = 52.8 bits (125), Expect = 2e-06
Identities = 22/41 (53%), Positives = 30/41 (73%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+K+++ +Y
Sbjct: 313 YAWPFYKPVDAEALHLDYHDIKHPMDLSTVKKKMSREY 353

☐ >gi|27804346|gb|AAO22237.1| BRD4-NUT fusion oncoprotein [Homo sapiens]
Length = 1846

Score = 87.4 bits (215), Expect = 9e-17
Identities = 39/49 (79%), Positives = 45/49 (91%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+R LE++Y
Sbjct: 71 LKTLWKHQFAWPFQQPVDAVKLNLPDYKIIKT'PMDMGTIKKR-LENNY 118

Score = 52.8 bits (125), Expect = 2e-06
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 372 YAWPFYKPDVEALGLHDYCDIHKPMDMSTIKSKLEAREY 412

☐ >gi|24640484|ref|NP_727228.1| ☒ CG2252-PA [Drosophila melanogaster]
gi|45554398|ref|NP_996368.1| CG2252-PE [Drosophila melanogaster]
gi|45554406|ref|NP_996369.1| CG2252-PD [Drosophila melanogaster]

gi|45554416|ref|NP_996370.1| CG2252-PC [Drosophila melanogaster]
gi|157455|gb|AAA28541.1| 5.9 kb fsh membrane protein
gi|22831926|gb|AAN09226.1| CG2252-PA [Drosophila melanogaster]
gi|45446848|gb|AAS65277.1| CG2252-PC [Drosophila melanogaster]
gi|45446849|gb|AAS65278.1| CG2252-PD [Drosophila melanogaster]
gi|45446850|gb|AAS65279.1| CG2252-PE [Drosophila melanogaster]
Length = 1110

Score = 87.4 bits (215), Expect = 9e-17
Identities = 38/49 (77%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
MK +WKH F+WPF+QPVDA KL LPDYHKIIKQPMDMGTIK+R LE++Y
Sbjct: 47 MKVIWKHHFSWPFQQPVDAKKLNLPDYHKIIKQPMDMGTIKKR-LENNY 94

Score = 60.8 bits (146), Expect = 7e-09
Identities = 27/45 (60%), Positives = 35/45 (77%), Gaps = 1/45 (2%)

Query: 6 KHQ-FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
KH +AWPF +PVDA LGL DYH IIK+PMD+GT+KR++ +Y
Sbjct: 495 KHSYGAWPFYKPVDAEMLGLHDYHDIKKPMDLGTVKKMDNREY 539

☐ >gi|31206311|ref|XP_312107.1| ENSANGP00000016848 [Anopheles gambiae]
gi|21295629|gb|EAA07774.1| ENSANGP00000016848 [Anopheles gambiae str. PEST]
Length = 806

Score = 87.0 bits (214), Expect = 1e-16
Identities = 39/49 (79%), Positives = 46/49 (93%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
MKA+WKHQF+WPF+QPVDA KL LPDYHKIIKQPM+GTIK+R LE++Y
Sbjct: 46 MKAVWKHQFSWPFQQPVDAKKLNLPDYHKIIKQPMDLGTIKKR-LENNY 93

Score = 58.9 bits (141), Expect = 3e-08
Identities = 25/41 (60%), Positives = 33/41 (80%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVDA LGL DYH IIK+PMD+GT+KR++ +Y
Sbjct: 427 YAWPFYKPVDAELLGLHDYHDIKKPMDLGTVKKMDNREY 467

☐ >gi|34853148|ref|XP_342397.1| similar to Brd3 protein [Rattus norvegicus]
Length = 659

Score = 86.3 bits (212), Expect = 2e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 47 VKTLWKHQFAWPFYQPVDAIKLNLPDYHKIIKNPMDMGTIKKR-LENNY 94

☐ >gi|48134425|ref|XP_393347.1| ☒ similar to ENSANGP00000016848 [Apis mellifera]
Length = 1488

Score = 86.3 bits (212), Expect = 2e-16
Identities = 38/49 (77%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K +WKHQFAWPF+QPVDA KL LPDYHKIIKQPMD+GTIK+R LE+ Y
Sbjct: 677 LKPVWKHQFAWPFQPVDAKLNLPDYHKIIKQPMDLGTIKKR-LENTY 724

Score = 57.8 bits (138), Expect = 6e-08
Identities = 26/45 (57%), Positives = 34/45 (75%), Gaps = 1/45 (2%)

Query: 6 KHQ-FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
KH +AWPF +PVDA LGL DYH IIK+PMD+GT+K ++ +Y
Sbjct: 1024 KHSYAWPFYKPVDAELLGLHDYHDIKKPMDLGTIVKTKMDNREY 1068

☐ >gi|26332152|dbj|BAC29806.1| ☒ unnamed protein product [Mus musculus]
Length = 511

Score = 85.5 bits (210), Expect = 3e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 46 VKTLWKHQFAWPFYQPVDAIKLNLPDYHKIIKNPMDMGTIKKR-LENNY 93

Score = 53.9 bits (128), Expect = 1e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 329 YAWPFYKPVDAEALHLDYHDIKHHPMDLSTVKKRMDSREY 369

☐ >gi|47115837|sp|Q8K2F0|BRD3_MOUSE ☒ Bromodomain-containing protein 3 (Bromodomain-containing protein FSRG2)
Length = 726

Score = 85.5 bits (210), Expect = 3e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 46 VKTLWKHQFAWPFYQPVDAIKLNLPDYHKIIKNPMDMGTIKKR-LENNY 93

Score = 53.9 bits (128), Expect = 1e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 329 YAWPFYKPVDAAEALHLDYHDIKHPMDLSTVKKRKMDSREY 369

☐ >[gi|31981064|ref|NP_075825.2|](#) ☒ bromodomain containing 3; bromodomain-containing
[gi|21594631|gb|AAH31536.1|](#) ☒ Bromodomain containing 3 [Mus musculus]
Length = 726

Score = 85.5 bits (210), Expect = 3e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 46 VKTLWKHQFAWPFYQPVDAIKLNLDPDYHKIIKNPMDMGTIKKR-LENNY 93

Score = 53.9 bits (128), Expect = 1e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 329 YAWPFYKPVDAAEALHLDYHDIKHPMDLSTVKKRKMDSREY 369

☐ >[gi|8575733|gb|AAF78072.1|](#) ☒ bromodomain-containing FSH-like protein FSRG2 [Mus]
Length = 726

Score = 85.5 bits (210), Expect = 3e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 46 VKTLWKHQFAWPFYQPVDAIKLNLDPDYHKIIKNPMDMGTIKKR-LENNY 93

Score = 53.9 bits (128), Expect = 1e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 329 YAWPFYKPVDAAEALHLDYHDIKHPMDLSTVKKRKMDSREY 369

☐ >[gi|40788944|dbj|BAA05393.2|](#) ☒ KIAA0043 [Homo sapiens]
Length = 731

Score = 85.1 bits (209), Expect = 4e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 52 VKTLWKHQFAWPFYQPVDAIKLNLDPDYHKIIKNPMDMGTIKKR-LENNY 99

Score = 53.1 bits (126), Expect = 2e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 335 YAWPFYKPVDAAEALHLDYHDIKHPMDLSTVKKRMDGREY 375

☐ >gi|21594670|gb|AAH32124.1| ☒ BRD3 protein [Homo sapiens]
Length = 556

Score = 85.1 bits (209), Expect = 4e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 47 VKTLWKHQFAWPFYQPVDAIKLNLDPDYHKIIKNPMDMGTIKKR-LENNY 94

Score = 52.8 bits (125), Expect = 2e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 330 YAWPFYKPVDAAEALHLDYHDIKHPMDLSTVKKRMDGREY 370

☐ >gi|26345416|dbj|BAC36359.1| ☒ unnamed protein product [Mus musculus]
Length = 505

Score = 85.1 bits (209), Expect = 4e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 46 VKTLWKHQFAWPFYQPVDAIKLNLDPDYHKIIKNPMDMGTIKKR-LENNY 93

Score = 53.5 bits (127), Expect = 1e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 329 YAWPFYKPVDAAEALHLDYHDIKHPMDLSTVKKRMDGREY 369

☐ >gi|11067749|ref|NP_031397.1| ☒ bromodomain containing protein 3; RING3-like gen
bromodomain-containing 3; open reading frame X [Homo
sapiens]



gi|12643726|sp|Q15059|BRD3 HUMAN ☒ Bromodomain-containing protein 3 (RING3-like p
Length = 726

Score = 85.1 bits (209), Expect = 4e-16
Identities = 39/49 (79%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF QPVDA+KL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 47 VKTLWKHQFAWPFYQPVDAIKLNLDPDYHKIIKNPMDMGTIKKR-LENNY 94

Score = 52.8 bits (125), Expect = 2e-06
Identities = 23/41 (56%), Positives = 30/41 (73%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ T+KR++ +Y
Sbjct: 330 YAWPFYKPVDAEALHLDYHDIKHMPDLSTVKKRMDGREY 370





 >gi|3184498|gb|AAC27978.1|  R31546_1 [Homo sapiens]
Length = 731

Score = 83.6 bits (205), Expect = 1e-15
Identities = 39/49 (79%), Positives = 45/49 (91%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+R LE++Y
Sbjct: 82 LKTLWKHQFAWPFQQPVDAVKLNLDPYYKIIKTPMDMGTIKKR-LENNY 129

Score = 50.8 bits (120), Expect = 9e-06
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 383 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLEAREY 423

 >gi|37674287|ref|NP_932762.1|  bromodomain containing 4 isoform 2; bromodomain-
bromodomain-containing 4 [Mus musculus]
 gi|18308127|gb|AAL67834.1|  bromodomain-containing protein BRD4 short variant [M]
Length = 723

Score = 83.2 bits (204), Expect = 1e-15
Identities = 39/49 (79%), Positives = 45/49 (91%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+R LE++Y
Sbjct: 71 LKTLWKHQFAWPFQQPVDAVKLNLDPYYKIIKTPMDMGTIKKR-LENNY 118

Score = 50.8 bits (120), Expect = 9e-06
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 373 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLESREY 413

□ >gi|7657218|ref|NP_055114.1| ■ bromodomain-containing protein 4 isoform short;
chromosome-associated protein; bromodomain-containing 4
[Homo sapiens]

gi|3115204|emb|CAA72780.1| ■ HUNKI [Homo sapiens]
Length = 722

Score = 83.2 bits (204), Expect = 1e-15
Identities = 39/49 (79%), Positives = 45/49 (91%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+R LE++Y
Sbjct: 71 LKTLWKHQFAWPFQQPVDAVKLNLPDYKIIKTPMDMGTIKKR-LENNY 118

Score = 50.4 bits (119), Expect = 1e-05
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 372 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLEAREY 412

□ >gi|45501005|gb|AAH67129.1| Unknown (protein for IMAGE:6138785) [Homo sapiens]
Length = 548

Score = 82.8 bits (203), Expect = 2e-15
Identities = 39/49 (79%), Positives = 45/49 (91%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+R LE++Y
Sbjct: 71 LKTLWKHQFAWPFQQPVDAVKLNLPDYKIIKTPMDMGTIKKR-LENNY 118

Score = 50.1 bits (118), Expect = 1e-05
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 372 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLEAREY 412

□ >gi|33879612|gb|AAH30158.1| ■ BRD4 protein [Homo sapiens]
Length = 548

Score = 82.8 bits (203), Expect = 2e-15
Identities = 39/49 (79%), Positives = 45/49 (91%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+R LE++Y
Sbjct: 71 LKTLWKHQFAWPFQQPVDAVKLNLPDYKIIKTPMDMGTIKKR-LENNY 118

Score = 50.1 bits (118), Expect = 1e-05
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 372 YAWPFYKPV DVEALGLHDYCDIIKHPMDMSTIKSKLEAREY 412

☐ >gi|33416361|gb|AAH55533.1| ☒ Zgc:77289 protein [Danio rerio]
Length = 499

Score = 82.4 bits (202), Expect = 2e-15
Identities = 37/49 (75%), Positives = 43/49 (87%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF PVDA+KL LPDYHK+IK PMDMGTIK+R LE++Y
Sbjct: 43 VKTLWKHQFAWPFYTPVDAIKLNLDPDYHKVIKNPMDMGTIKKR-LENNY 90

Score = 55.1 bits (131), Expect = 5e-07
Identities = 23/41 (56%), Positives = 32/41 (78%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH+IIKQPM+ T+K+++ +Y
Sbjct: 313 YAWPFYKPVDAEALHLDYHEIIKQPMDLSTVKKKMSREY 353

☐ >gi|47086635|ref|NP_997867.1| ☒ Unknown (protein for MGC:77289); wu:fa28f05 [Dan
gi|41944567|gb|AAH65949.1| ☒ Unknown (protein for MGC:77289) [Danio rerio]
Length = 664

Score = 82.4 bits (202), Expect = 3e-15
Identities = 37/49 (75%), Positives = 43/49 (87%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF PVDA+KL LPDYHK+IK PMDMGTIK+R LE++Y
Sbjct: 43 VKTLWKHQFAWPFYTPVDAIKLNLDPDYHKVIKNPMDMGTIKKR-LENNY 90

Score = 55.1 bits (131), Expect = 5e-07
Identities = 23/41 (56%), Positives = 32/41 (78%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH+IIKQPM+ T+K+++ +Y
Sbjct: 313 YAWPFYKPVDAEALHLDYHEIIKQPMDLSTVKKKMSREY 353

☐ >gi|33417197|gb|AAH55508.1| Unknown (protein for IMAGE:3819162) [Danio rerio]
Length = 558

Score = 82.0 bits (201), Expect = 3e-15
Identities = 37/49 (75%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+KALW+H FAWPF +PVDA +L LPDYHKIIKQPMDMGTIK+R LE++Y
Sbjct: 61 VKALWRHHFAWPFHEPVDATRLNLPDYHKIIKQPMDMGTIKR-LENNY 108

Score = 58.5 bits (140), Expect = 4e-08
Identities = 26/41 (63%), Positives = 32/41 (78%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA LGL DYH IIK PMD+ TIKR++ E +Y
Sbjct: 358 YAWPFYKPVDAALGLHDYHDIKHPMDLSTIKRKMDEREY 398

☐ >gi|47216871|emb|CAG11678.1| unnamed protein product [Tetraodon nigroviridis]
Length = 834

Score = 82.0 bits (201), Expect = 3e-15
Identities = 37/49 (75%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K+LW+H FAWPF +PVDAVKL LPDYHKIIK PMDMGTIK+R LE++Y
Sbjct: 60 LKSLWRHHFAWPFHEPVDVKLNLPDYHKIIKTPMDMGTIKR-LENNY 107

Score = 58.9 bits (141), Expect = 3e-08
Identities = 26/41 (63%), Positives = 32/41 (78%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA LGL DYH IIKQPMD+ TIKR++ +Y
Sbjct: 423 YAWPFYKPVDAASSLGLHDYHDIKQPMDLSTIKRKMDNREY 463

☐ >gi|19171509|emb|CAC84085.1| hypothetical protein [Takifugu rubripes]
Length = 701

Score = 81.3 bits (199), Expect = 6e-15
Identities = 37/49 (75%), Positives = 43/49 (87%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF QPVDA+KL L DYHK+IK PMDMGTIK+R LE++Y
Sbjct: 44 VKTLWKHQFAWPFYQPVDAIKLCLADYHKVIKNPMDMGTIKR-LENNY 91

Score = 52.8 bits (125), Expect = 2e-06
Identities = 22/41 (53%), Positives = 31/41 (75%)

Query: 9 FAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ TI++++ + +Y
Sbjct: 315 YAWPFYKPVDAEALGLHDYHDIKHPMDLSTIRKKMDKGEY 355

☐ >gi|34862361|ref|XP_343176.1| ☒ similar to bromodomain-containing protein BRD4 s
[Rattus norvegicus]




Length = 1433

Score = 80.9 bits (198), Expect = 7e-15
Identities = 38/49 (77%), Positives = 43/49 (87%)

Query: 1 MKALWKHQFAWPFQRPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+RL + Y
Sbjct: 71 LKTLWKHQFAWPFQRPVDAVKLNLPDYKIIKTPMDMGTIKKRLNNYY 119

Score = 49.3 bits (116), Expect = 2e-05
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFQRPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 373 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLESREY 413


☐ >[gi|19718731|ref|NP_490597.1|](#)  bromodomain-containing protein 4 isoform long;
chromosome-associated protein; bromodomain-containing 4
[Homo sapiens]
[gi|20141192|sp|O60885|BRD4 HUMAN](#)  Bromodomain-containing protein 4 (HUNK1 protei
[gi|16589003|gb|AAL26987.1|](#)  bromodomain-containing 4 [Homo sapiens]
Length = 1362

Score = 80.9 bits (198), Expect = 8e-15
Identities = 38/49 (77%), Positives = 43/49 (87%)

Query: 1 MKALWKHQFAWPFQRPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+RL + Y
Sbjct: 71 LKTLWKHQFAWPFQRPVDAVKLNLPDYKIIKTPMDMGTIKKRLNNYY 119

Score = 48.9 bits (115), Expect = 3e-05
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFQRPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 372 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLEAREY 412

☐ >[gi|9931486|gb|AAG02191.1|](#)  cell proliferation related protein CAP [Mus musculu
Length = 1400

Score = 80.5 bits (197), Expect = 9e-15
Identities = 38/49 (77%), Positives = 43/49 (87%)

Query: 1 MKALWKHQFAWPFQRPVDAVKLGLPDYHKIIKQPMDMGTIKRRLLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+RL + Y
Sbjct: 71 LKTLWKHQFAWPFQRPVDAVKLNLPDYKIIKTPMDMGTIKKRLNNYY 119

Score = 49.3 bits (116), Expect = 3e-05
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 373 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLESREY 413

☐ >[gi|31560788|ref|NP_065254.2|](#) ☒ bromodomain containing 4 isoform 1; bromodomain-
bromodomain-containing 4 [Mus musculus]
[gi|18308125|gb|AAL67833.1|](#) ☒ bromodomain-containing protein BRD4 long variant [Mu
Length = 1400

Score = 80.5 bits (197), Expect = 9e-15
Identities = 38/49 (77%), Positives = 43/49 (87%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K LWKHQFAWPF+QPVDAVKL LPDY+KIIK PMDMGTIK+RL + Y
Sbjct: 71 LKTLWKHQFAWPFQPVDAVKLNLPDYKIIKTPMDMGTIKKRENNYY 119

Score = 49.3 bits (116), Expect = 3e-05
Identities = 24/41 (58%), Positives = 28/41 (68%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVD LGL DY IIK PMDM TIK +L +Y
Sbjct: 373 YAWPFYKPVDEALGLHDYCDIIKHPMDMSTIKSKLESREY 413

☐ >[gi|47210026|emb|CAF90901.1|](#) unnamed protein product [Tetraodon nigroviridis]
Length = 1594

Score = 80.5 bits (197), Expect = 1e-14
Identities = 38/49 (77%), Positives = 44/49 (89%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K+LWKH FAWPF+ PVDVKL LPDY+KIIK PMDMGTIKRR LE++Y
Sbjct: 468 LKSLWKHHFAWPFQAPVDAVKLNLPDYKIIKTPMDMGTIKRR-LENNY 515

Score = 51.6 bits (122), Expect = 5e-06
Identities = 22/41 (53%), Positives = 29/41 (70%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVD LGL DY+ IIK PMD+ TIK+++ Y
Sbjct: 763 YAWPFYKPVDTVSLGLHDYYDIIKHPMDLSTIKKKMDSRQY 803

☐ >[gi|18157527|dbj|BAB83842.1|](#) BRD2~partially supported by GENSCAN and GraileXP [O
Length = 814

Score = 79.3 bits (194), Expect = 2e-14
Identities = 35/49 (71%), Positives = 43/49 (87%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K+LW+H FAWPF +PVDA KL LPDYHKIIK PMDMGTI++R LE++Y

Sbjct: 86 LKSLWRHHFAWPFHEPVDAAKLNLDPYHKIIKTPMDMGTIKRKR-LENNY 133

Score = 57.8 bits (138), Expect = 7e-08
Identities = 26/41 (63%), Positives = 33/41 (80%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVDAV LGL DYH+IIK PMD+ TIKR++ +Y
Sbjct: 401 YAWPFYKPVDAVSLGLHDYHEIIKFPMDLSTIKRKMDGREY 441

☐ >gi|47212213|emb|CAF94980.1| unnamed protein product [Tetraodon nigroviridis]
Length = 642

Score = 79.0 bits (193), Expect = 3e-14
Identities = 37/49 (75%), Positives = 43/49 (87%), Gaps = 1/49 (2%)

Query: 1 MKALWKHQFAWPFQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+K LWKHQFAWPF QPVDA+KL L DYHK+IK PMDMGTIK+R LE++Y
Sbjct: 28 VKTLWKHQFAWPFYQPVDAIKLCLADYHKVIKNPMDMGTIKKR-LENNY 75

Score = 51.6 bits (122), Expect = 5e-06
Identities = 22/41 (53%), Positives = 31/41 (75%)

Query: 9 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRILLEDDY 49
+AWPF +PVDA L L DYH IIK PMD+ TI++++ + +Y
Sbjct: 305 YAWPFYKPVDAEAELELHDYHDIKHPMDLSTIRKKMDKGEY 345

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
Posted date: Jul 7, 2004 11:55 PM
Number of letters in database: 640,719,545
Number of sequences in database: 1,921,076

Lambda	K	H
0.326	0.142	0.476

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 16,291,769
Number of Sequences: 1921076
Number of extensions: 439624
Number of successful extensions: 1198
Number of sequences better than 10.0: 127

Number of HSP's better than 10.0 without gapping: 93
Number of HSP's successfully gapped in prelim test: 34
Number of HSP's that attempted gapping in prelim test: 1011
Number of HSP's gapped (non-prelim): 181
length of query: 49
length of database: 640,719,545
effective HSP length: 22
effective length of query: 27
effective length of database: 598,455,873
effective search space: 16158308571
effective search space used: 16158308571
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.6 bits)
S2: 68 (30.8 bits)



Conserved Domain Database

PubMed

Nucleotide

Protein

Structure

CDD

Taxonomy

Help?

CD: **COG5076.1, COG5076**

PSSM-Id: 14205

Source: **Cog**

Description: Transcription factor involved in chromatin remodeling, contains bromodomain [Chromatin structure and dynamics / Transcription]

Taxa: **Eukaryota**

Related: may span multiple domains

Status: Alignment from source

Created: 7-Oct-2002

Aligned: 22 rows

PSSM: 371 columns

Representative: Consensus

Proteins: [\[Click here for CDART summary of Proteins containing COG5076\]](#)

View Alignment

as **Hypertext**width **60**color at **2.0 bits**

Subset Rows

up to **10**

of the most diverse members

	10	20	30	40	50	60
consensus	1	1	1	1	1	1
gi 19173481	1	1	1	1	1	1
gi 19173489	1	1	1	1	1	1
gi 19074752	1	1	1	1	1	1
gi 19114532	70	1	1	1	1	1
gi 12229701	1	1	1	1	1	1
gi 19112795	1	1	1	1	1	1
gi 1723670	115	1	1	1	1	1
gi 401643	40	1	1	1	1	1
gi 5921175	1	1	1	1	1	1
	70	80	90	100	110	120
consensus	59	1	1	1	1	1
gi 19173481	1	1	1	1	1	1
gi 19173489	61	1	1	1	1	1
gi 19074752	61	1	1	1	1	1
gi 19114532	120	1	1	1	1	1
gi 12229701	56	1	1	1	1	1
gi 19112795	42	1	1	1	1	1
gi 1723670	167	1	1	1	1	1
gi 401643	100	1	1	1	1	1
gi 5921175	60	1	1	1	1	1
	130	140	150	160	170	180
consensus	117	1	1	1	1	1
gi 19173481	19	1	1	1	1	1
gi 19173489	121	1	1	1	1	1
gi 19074752	114	1	1	1	1	1
gi 19114532	190	1	1	1	1	1
gi 12229701	115	1	1	1	1	1
gi 19112795	102	1	1	1	1	1
gi 1723670	212	1	1	1	1	1
gi 401643	160	1	1	1	1	1
gi 5921175	120	1	1	1	1	1
	190	200	210	220	230	240
consensus	142	1	1	1	1	1
gi 19173481	40	1	1	1	1	1

gi_19173489	149	MKAEDYEFCSSETLSDLVKPKHKAYNWPFLPEVPGDLVPGIYSVIKEP-MDLQTMRSKLEQ	207
gi_19074752	174	VTYADNFAIGYFRKQGFSTDVRFGG--WISFIKUYEGGTVECCVSWeINYLNKQETTES	231
gi_19114532	229	EMTKEQHKYITHAMLRQLRRGRDSIPFRAPVDVPVKQNIPTDPTTIKNP-IDLGTMQKKFSS	287
gi_12229701	143	DVPKVIQNILDALHEEKDEQGRFLIDIFIDLPSCRILYFDYEBIISKSP-MTIKMLEKRFKK	201
gi_19112795	122	LALBEADKEAKKAKTEAPVEAANKSLRSRKKTFEIAAFANIEPEVAPETKTTPKKRAALSN	181
gi_1723670	236	PYVLRITKNILKMMRREVDQNNKTLTLCFEKLPDRNBEPTIYYSVITDE-ICLMDIRKKVKS	294
gi_401643	186	TEKINQALLGASSPKNLDDKVKLSEPFMELNDKDELPEYFEIVHSP-MALSIVKQNLFI	244
gi_5921175	148	PIPKHQQKHALLAIAKAVRRLKIDARFLLQPVDFVFLDIPFYFN7IKRP-MDLSTIERKLN	206
		250 260 270 280 290 300	
	*.....*.....*.....*.....*.....*.....	
consensus	201	GRYKSFEEFVSDNLNMFNCKLYN-GPDSSVYVDAKELEKYFLKLIIEIPEEMLELSIKP	259
gi_19173481	98	--KYKSFEEFKADLDLIWDNCLRFD-QEKHHRPCATKMRREVSTFEIEVVPVCMDEGFFPMN	155
gi_19173489	208	RRYQSVVEEFGRLDELIVENCKKFN-APGTEVYVCGQEFKAVKMMHMQKVSPhDIKSRITE	266
gi_19074752	232	MRRKLFEEMKGINNYHIT---HK---IEDYS---RIKEIGDIPOVSGVECEIVEEDRGMRLQA	284
gi_19114532	288	GVYSSAQHFIDIPNLMFNSCNFLYN-GTESPVGVMGKNLQATFERQLKQLPSAYVTSYSRP	346
gi_12229701	202	GEYTTLESFVKDLNQMFNANTYN-APGSFVIEDAEKLSQLSSSLISSFSEQPKHSPAT	260
gi_19112795	182	BEKQSLKFKQSAMLEPMLDNISNRHFGAPESHVPNRKEAPDYDSLVIKPODLRTLENMIKE	241
gi_1723670	295	PKYRNFTFEEDFQULLENFKLIY-SQDQSNLIRAQLLEKNENRILVR-IELSKPDEDYLP	352
gi_401643	243	GQYSKIYDFIEMLLVFQNAHIFN-DPSALIYKDATTITNYFNLYLIQKETTPELQDLNER	303
gi_5921175	207	GAYEVPEQITEDFNLMVNNSIKFN-GPNAGISQMARNIQASFEKHMNMMPAKDAPPVIAK	265
		310 320 330 340 350 360	
	*.....*.....*.....*.....*.....*.....	
consensus	260	GR-EEREE-----RESVLITNS---QAHVGAWPFLEPVSDDEVEDDYKDIRDPMD	305
gi_19173481	156	SSiWEGGEn-----QGFCIKHAIrkMAARVLLSTGYGEASRTALWVLCDAFQRKML	206
gi_19173489	267	LK-RKVMSy-----sREIRMLESKI---MEQTGEMPTSRAYSINERVSIGNAILNMSK	315
gi_19074752	283	R-----FISYLLISDL---QSNAAWPFLLRPVDPAEVDPDYKCIAPMD	324
gi_19114532	347	GR-RPRSMtpakggartRQAAMYSNSs---SGIRETMYDLKPHRRKDAEMKFCQSVLKE	403
gi_12229701	261	SK-HEPEE-----TPASPTFSV---SASTSRERSTSVAPSFITSDQAATPDVLKS	306
gi_19112795	242	GNITEVDEL-----yREVLRIFANckmYNGSDPANAMSIWGLECFRYTEELEDIYRQ	293
gi_1723670	353	EG-ELRYP-----LDDVEINDE---KYQIGDWVLLHNPNDINKPIVGQIFERLWST	398
gi_401643	304	GE-INLEFdkf-----eFENYLAIGGGg---PAAAGALAI SLDNDIEPESNRDLIDQAD	355
gi_5921175	266	GR-----RSSAQEDAP---IVIRRAQTHNGRPKKTIHPPKSKDIYPYES	306
		370 380 390 400 410 420	
	*.....*.....*.....*.....*.....*.....	
consensus	306	LSTKELK-LRNNYRFE-ETFVRDAKLFFDNCVMYNGEVTDYTKMANVLEDFVIKKTRLI	363
gi_19173481	207	ELINEVVAEPAGG-----	219
gi_19173489	316	EQTESVAKIVLKNAGAGEFVENDEIEVDMRTIPDHVVEEIDMYIKSINVGEDVRDE-----	370
gi_19074752	325	LSTMVLK-LRNNEYGCI-EAFVADVHLMVNNCFEYNGRDTQYYKCAQALLDHFNKKLEFY	382
gi_19114532	404	LLKKQHEaYAYFFYKVPnPTACGCPDYFKVIKHPMDLGTMQNKLNRNEYASMKAFEDMV	463
gi_12229701	307	EEARVES-FSKESNDQ-TPIPEDVPSMDTILSQANYGAFALIKSFPSTPVPDFLNFESHK	364
gi_19112795	294	ASTRSQ-----	299
gi_1723670	399	TDGNKWL-NACWYFRPE-QTVHVPDRLFYKNEVMKTCQYRDHPIQDINGKCYVINFTRFQ	456
gi_401643	356	YDENHFEgLGNGYNRLITEDYLLNPNNEFKKLIAPETVQSEVKNERSTTSDIKTNLSL	415
gi_5921175	307	KKPKSKR-LQQAMKFCQ=VLKELNAKKEHASYNYPFLEPVDFVSMNLPTYFDYVKEFMDLG	365
	*.....	
consensus	364	REYPKLID 371	
gi_19173481		-----	
gi_19173489		-----	
gi_19074752	383	RAVVGRLS 390	
gi_19114532	464	LMFKNCYK 471	
gi_12229701	365	SVMGRSTF 372	
gi_19112795		-----	
gi_1723670	457	RGDESTFV 464	
gi_401643	416	SEHLKIPK 423	
gi_5921175	366	TIACKLND 373	

Citing CDD: Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR,

Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen PA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, Bryant SH (2003), "*CDD: a curated Entrez database of conserved domain alignments*", **Nucleic Acids Res.** **31**: 383-387

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Conserved Domain Database

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 [Structure](#)
 [CDD](#)
 [Taxonomy](#)
 [Help?](#)

CD: [pfam00439.11](#) **Bromodomain** PSSM-Id: 22994

Source: [Pfam\[US\]](#), [Pfam\[UK\]](#)

Description: Bromodomain. Bromodomains are 110 amino acid long domains, that are found in many chromatin associated proteins. Bromodomains can interact specifically with acetylated lysine.

Taxa: [Eukaryota](#)

References: [3 PubMed Links](#)

Related: [smari00297](#)

Status: Alignment from source

Created: 12-Dec-2003

Aligned: 68 rows

PSSM: 91 columns

Representative: Consensus

Proteins: [\[Click here for CDART summary of Proteins containing pfam00439\]](#)

[View 3D Structure](#) with [Cn3D](#) using [Virtual Bonds](#) (To display structure, download [Cn3D](#))

[View Alignment](#) as [Hypertext](#) width 60 color at [2.0 bits](#)

[Subset Rows](#) up to 10 of the most diverse members

		10	20	30	40	50	60	
	******	
consensus	1	LNKLLLVLEALDENDPRSLF	FLFPVLPS	LEVPDY	YEIIKKPMDL	KTIKKL	KNGKYSS 60	
1E61_A	13	PHDAATQNIILTELQNHA	AAWPF	LQPVNKE--	EVPDYDFI	KEPMDL	STMEIKLESNKYQK 70	
gi_1729862	1003	GDATFLVHLFEPETSDN	FNWQPAYIK	DENMI	LEVSTGR	KFFN--	MDLDIVEERLWNGYYSE 1060	
gi_2443880	256	LPKELMKIYNTIAQN---	ECALVFR	RRLD	qKRG	RYKKLV	RRRMDLDTVQSRINGCSISS 312	
gi_3560213	190	FQSAMPLMLDNISNHR-	FGAPFS	HPVNRK---	EAPDYD	SLVYK	PPQDLRTLKNMIKEGNITE 246	
gi_1431082	138	QSKYLLSSIKATKRLK-	DARPF	LKPV	DFIa	LNITHY	FNYVQTFMDLSLIETKLQGNVYHS 196	
gi_401643	58	FNRFISFTLDVLIDKY-	KDIFK	DFIK	LPS	ckFHP	QYVYKIQQFMSINETKSRDYEYE--DG 115	
gi_18958139	46	GNVYMAQIRKHRSSAG	NNSVF	ESTL	ALP	FF	FEPEYVEQVKEPIDVTTTQHKLKIPEYLT 105	
gi_12230583	281	MKNVMKVLKKEVLD-	SGIGL	FDL	FER	LPD	chRDANYVIMIANPISLQIINKVKTRRYKT 339	
gi_30173008	508	ERGFKPTELLCQEVIE	ALKTT	DAGK	VFA	p	v	LVGYTDIIENPICLKIMSEKAASGKYST 567
		70	80	90				
	******	
consensus	61	PEEFVADFNLMFSKARTY	NEPDSE	VYKD	ANK		91	
1E61_A	71	MEDFIYDARLVFN	NCRMY	NGENTS	YYYK	YANR	101	
gi_1729862	1061	PKQFLKDIELIYRD	ANTIGD	RRE	VIK	ASEMF	1091	
gi_2443880	313	AKELFRDPELLVAN	NAAI	FYSK	N	TREYK	SAVG 343	
gi_3560213	247	VDELYREVLRI	FANCK	MYNG	S	DPANAM	STWG 277	
gi_1431082	197	VEQVTSDFKTM	VDNCL	NFNG	P	ESSISS	MAKR 227	
gi_401643	116	PSNFELLOVELE	TKNC	QAYN	EYD	SLIV	NSMQ 146	
gi_18958139	106	YDQFNDDFM	FIKNN	LFY	KD	ESEEH	NMMK 136	
gi_12230583	340	FQEFQNDENL	MLTN	FRISH	R	GDPE	SINISNI 370	
gi_30173008	568	VAALSADVQLN	LSNCA	FFNK	GN	EVYIK	YGNT 598	

Citing CDD: Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen PA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, Bryant SH (2003), "CDD: a curated Entrez database of conserved domain alignments", *Nucleic Acids Res.* 31: 383-387

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Conserved Domain Database

PubMed Nucleotide Protein Structure CDD Taxonomy Help?

CD: [smart00297.10](#) **BROMO**

PSSM-Id: 22746

Source: [Smart](#)

Description: bromo domain;

Taxa: [Eukaryota](#)

References: [2 Pubmed Links](#)

Related: [pfam00439](#)

Status: Alignment from source

Created: 12-Dec-2003

Aligned: 78 rows

PSSM: 109 columns

Representative: Consensus

Proteins: [\[Click here for CDART summary of Proteins containing smart00297\]](#)

View 3D Structure with [Cn3D](#) using [Virtual Bonds](#) (To display structure, download [Cn3D](#))

View Alignment as [Hypertext](#) width 60 color at [2.0 bits](#)

Subset Rows [up to 10](#) of the most diverse members

		10	20	30	40	50	60	
consensus	1	SPKLQKKLQELLKAVLDKLDSE	-----	PLSWPFL	29			
IE6I_A	7	QRPKRGPDAAIQNTILTELQNH	-----	AAAWPFL	35			
gi_1699027	697	SPANQRKCERVLALFCHPCF	-----	FLH	721			
gi_627837	1538	RLALEKELQASLKQVLTALINS	rutshllryrqaakppdlnpeteesipr	ssP	EGPDP	1597		
gi_22135972	1416	REKLLSLFAGLVKSISKHQDSY	-----	GIQ	1440			
gi_2443880	249	SRGSLALPKELMKIYNTIAQN	-----	ECALNFR	277			
gi_3560213	183	EKQSLKKFQSAMLFMLDNISNH	-----	RFGAPFS	211			
gi_3702343	952	IQKRCKIVISKLQRRIDKEGQQiv	-----	pmLT	979			
gi_6226901	863	FEHVIEKINTPPKVFDPRIMRD	-----	RRFVEEV	891			
gi_951231	773	TLIIQELIHNLFSVSMHQDEg	-----	rcYSDSLA	803			
		70	80	90	100	110	120	
consensus	30	KPVSRRKEAPDYDIIKKPMDLKT	IKKKLENGKY	-----	RSVEEFVADFNLMFSNARTYNG	--	84	
IE6I_A	36	QPVNKEEVDPDYDFIKPMDLST	MEIKLESNKY	-----	QKMEDFIYDARLVFNNCRMNG	--	90	
gi_1699027	722	QLATDST	---FSLDQFGGTLTLTLRLARL	QEKLS	pppySSSQEFAQDVGRMF	KQFNKLT	---	776
gi_627837	1598	VLTEVSK	-----	QDEQQPLDLEGVKKFMDQGSY	---VSVLEFSDDIVKLIQ	AAINSDg	---	1647
gi_22135972	1441	KLNEAAQKMFDFCNREFVFLY	PELIHERLENQYY	---RSIESFKHDVDAMLSNAEL	YFV	---	1498	
gi_2443880	278	RRLDSQKRGYKKLVRRMDLDT	VQSRINGCSI	---SSAKELFRDFLLVANNAAI	FYS	---	332	
gi_3560213	212	HFVNKEAPDYDSLVIKQQLRT	LKNMIREGNI	---TEVDELYREVLRI	FANCKMYNGsd	---	268	
gi_3702343	980	NLWKRIQNGYAAGGVNMLLE	LRIDHRVERLEY	---AGVMELASDVQMLR	GAMQTYG	---	1034	
gi_6226901	892	EPVDPDEAEEDYELIETPIC	MDIMEKLNCEY	---NHADKEVADLILIQTNAL	EYNP	---	946	
gi_951231	804	EIPAVDP	---NFPNKPPLTFDIIRKNVEN	NRY	---RRLDLFQENMFVLERARR	MNR	---	354
		130	140					
consensus	85	PDSEVYKDAKKLEKFFTEKKL	RELP	109				
IE6I_A	91	ENTSYKYANKLEKFFNNKVKE	LEPE	115				
gi_1699027	777	EDKADVQSIIGLQRFETTRM	NEATG	801				
gi_627837	1648	GQPEIKNANSMVKSFFTRQ	MERVEP	1672				
gi_22135972	1496	RSAMLSKIKRLRDKLT	TKLPKLI	1519				
gi_2443880	333	KNTREYKSAVGLRDIVTK	SLPHYL	357				
gi_3560213	269	PANAMSIWGDECFRYTEEL	FUIYRQ	293				
gi_3702343	1035	FSHEVRSEAKNVHNLFFDL	LKMSFP	1059				
gi_6226901	947	STTKDGKLIHQMANTLRDA	IDDLIE	971				
gi_951231	855	TDSEIYEDAVELQQFFIKIR	DELCK	879				

Citing CDD: Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan

V, Song JS, Thiessen PA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, Bryant SH (2003), "*CDD: a curated Entrez database of conserved domain alignments*", *Nucleic Acids Res.* **31**: 383-387

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